

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 8, 2002, 09:30:40 ; Search time 25.41 Seconds
(without alignments) 211.767 Million cell updates/sec

Title: US-09-640-211a-2347

Perfect score: 307

Sequence: 1 PDVRRGNITTEEDLLIMELHSHKNGNRSKIAKILPGRTONEIKNFWTRIOKHIKO 56

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298	97.1	217	2	T06455 Myb26 protein - ga
2	287.5	93.6	198	1	JQ0959 myb-related protei
3	281	91.5	205	1	JQ0958 myb-related protei
4	279	90.9	333	2	T09736 myb-related protei
5	279	90.9	333	2	T09735 ABA-induced myb-re
6	279	90.9	333	2	T09737 dehydration-induce
7	259	84.4	286	2	H96706 myb-related
8	259	84.4	293	2	T09758 myb-related
9	255	83.1	216	2	D96520 myb-related
10	254	82.7	278	2	C86383 hypothetical prote
11	246	80.1	273	1	JQ2330 probable Myb-like
12	225	73.3	141	2	T51642 Myb transcription
13	217	70.7	261	2	T06650 probable transcrip
14	215	70.0	234	2	T51642 myb-related protei
15	215	70.0	256	2	T49254 myb-related transc
16	210	68.4	218	2	T51681 myb DNA binding pr
17	205	66.8	118	2	T51684 myb-related transc
18	203	66.1	204	2	T51689 myb-related transc
19	196	63.8	274	2	T07393 myb-related transc
20	195	63.5	327	2	T01038 myb-related protei
21	195	63.5	331	1	S69190 myb-related protei
22	194	63.2	238	2	T46166 MYB27 protein - Ar
23	194	63.2	268	1	JQ0961 myb-related protei
24	194	63.2	378	2	T51647 myb-related transc
25	192	62.5	414	2	A86229 hypothetical prote
26	190	61.9	217	2	T51671 myb-related transc
27	190	61.9	282	2	C96687 hypothetical prote
28	190	61.9	376	2	T03988 myb-like transcrip
29	190	61.9	399	1	A39697 maize myb-related

30	190	61.9	553	2	T03762 myb-related transc
31	189	61.6	203	2	T51653 myb-related transc
32	189	61.6	263	2	T48607 probable transcrip
33	189	61.6	370	2	C96664 hypothetical protei
34	189	61.6	553	2	T06179 myb-related protei
35	188	61.2	265	2	T07395 myb-related transc
36	188	61.2	280	1	S26604 myb-related protei
37	188	61.2	325	2	T53509 myb-related transcrip
38	188	61.2	421	1	S24244 myb-related protei
39	188	61.2	745	2	A71448 probable MYB trans
40	187	60.9	274	2	D86300 hypothetical prote
41	187	60.9	278	2	T03850 myb-related protei
42	186	60.6	279	2	T03830 probable myb facto
43	186	60.6	1297	2	T52065 probable myb-relat
44	185	60.3	369	2	T01196 transcripion fact
45	185	60.3	371	2	T00438 probable MYB famill

ALIGNMENTS

RESULT 1
T06455
Myb26 protein - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C:Accession: T06455
R:Umarl, A.; Strommer, J.
Plant J. 12, 1273-1284, 1997
A:Title: Myb26: A MYB-like protein of pea flowers with affinity for promoters of phen
A:Reference number: Z15690; X01D:98112025
A:Accession: T06455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-217 <UIM>
A:Cross-references: EMBL:Y11105; NID:q1841474; PIDN:CAAT1997.1; PID:q1841475
C:Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology
C:Keywords: DNA binding
F:11-63/Domain: myb DNA-binding repeat homology <MYB>
F:64-113/Domain: myb DNA-binding repeat homology <MYB1>

Query Match 97.1%; Score 298; DB 2; Length 217;
Best Local Similarity 96.4%; Pred. No. 1.3e-28;
Matches 54; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PDVRRGNITTEEDLLIMELHSHKNGNRSKIAKILPGRTONEIKNFWTRIOKHIKO 56
DB 65 PDVRRGNITTEEDLLIMELHSHKNGNRSKIAKILPGRTONEIKNFWTRIOKHIKO 120

RESULT 2
JQ0959
myb-related protein 340 - garden snapdragon
C:Species: Antirrhinum majus (garden snapdragon)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 02-Sep-1997
C:Accession: JQ0959
R:Jackson, D.; Cullane-Macle, F.; Prescott, A.G.; Roberts, K.; Martin, C.
Plant Cell 3, 115-125, 1991
A:Title: Expression patterns of myb genes from Antirrhinum flowers.
A:Reference number: JQ0956; M01D:93005689
A:Accession: JQ0959
A:Molecule type: mRNA
A:Residues: 1-198 <JAC>
A:Experimental source: strain JI-522
C:Comment: This protein is specifically expressed in flowers.
C:Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology
C:Keywords: DNA binding; duplication
F:10-62/Domain: myb DNA-binding repeat homology <MYB1>
F:63-113/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 93.6%; Score 287.5; DB 1; Length 198;

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719

A:Accession: H96706
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-286 <STO>
 A:Cross-references: GB:AE005173; NID:g6715735; PIDN:AAF26496.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: T22E19.5
 A:Map position: 1
 C:Superfamily: maize myb-related protein 1; myb DNA-binding repeat homology

Query Match 84.4%; Score 259; DB 2; Length 286;
 Best Local Similarity 76.8%; Pred. No. 9e-24;
 Matches 43; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PDVRCNITTEEDLLIMELHAKGNRMSKIAKHLPGRTDNEIKNFWRTRIOKHIO 56
 Db 70 PDIRGNLTPOEQLLIELHSMGNRMSKIAQYLPGRDNEIKNFWRTRIOKARO 125

RESULT 8
 T09758
 myb-related protein - upland cotton
 N:Alternate names: MYB-like DNA-binding domain protein
 C:Species: *Gossypium hirsutum* (upland cotton)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
 C:Accession: T09758
 R:Loguercio, L.L.; Zhang, J.; Wilkins, T.A.
 submitted to the EMBL Data Library, November 1997
 A:Description: Structure and expression of six classes of myb-domain genes in allotetrap
 A:Reference number: Z16842
 A:Accession: T09758
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-293 <LOG>
 A:Cross-references: EMBL:AF034133; NID:g2921337; PID:g2921338
 A:Experimental source: cultivar Acala SD-2; ovule
 C:Genetics:
 A:Note: CmY-N
 C:Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology
 C:Keywords: DNA binding; transcription regulation
 F:70-119/Domain: myb DNA-binding repeat homology <MYB>

Query Match 84.4%; Score 259; DB 2; Length 293;
 Best Local Similarity 76.8%; Pred. No. 9.3e-24;
 Matches 43; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PDVRCNITTEEDLLIMELHAKGNRMSKIAKHLPGRTDNEIKNFWRTRIOKHIO 56
 Db 71 PEIKRGNLTSEEDLLIELHSMGNRMSKIAQYLPGRDNEIKNFWRTRIOKARO 126

RESULT 9
 D96520
 hypothetical protein T2J15.9 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cross)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C:Accession: D96520
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719

A:Accession: D96520
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-216 <STO>
 A:Cross-references: GB:AE005173; NID:g10645470; PIDN:AMG21584.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: T2J15.9
 A:Map position: 1
 C:Superfamily: trichome differentiation protein GL1; myb DNA-binding repeat homology

Query Match 83.1%; Score 255; DB 2; Length 216;
 Best Local Similarity 74.5%; Pred. No. 2e-23;
 Matches 41; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PDVRCNITTEEDLLIMELHAKGNRMSKIAKHLPGRTDNEIKNFWRTRIOKHIO 55
 Db 56 PDIRGDISIQEQFIIEHSMGNRMSKIAQYLPGRDNEIKNFWRTRIOKAK 110

RESULT 10
 C86383
 probable Myb-like protein (Myb26) [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cross)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: C86383
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719
 A:Accession: C86383
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-278 <STO>
 A:Cross-references: GB:AE005172; NID:g11067290; PIDN:AAQ28618.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1
 C:Superfamily: anthocyanin biosynthesis regulatory protein; myb DNA-binding repeat ho

Query Match 82.7%; Score 254; DB 2; Length 278;
 Best Local Similarity 73.2%; Pred. No. 3.5e-23;
 Matches 41; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PDVRCNITTEEDLLIMELHAKGNRMSKIAKHLPGRTDNEIKNFWRTRIOKHIO 56
 Db 64 PDIRGNLTPOEQLLIELHSMGNRMSKIAQYLPGRDNEIKNFWRTRIOKARO 119

RESULT 11
 J02390
 MYB transcription factor (Atmyb2) [imported] - *Arabidopsis thaliana*
 N:Alternate names: myb-related protein 2; AtMYB2 protein
 C:Species: *Arabidopsis thaliana* (mouse-ear cross)
 C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 23-Mar-2001
 C:Accession: J02390; B84912
 R:Urao, T.; Yamaguchi-Shinozaki, K.; Urao, S.; Shinozaki, K.
 Plant Cell 5, 1529-1539, 1993
 A:Title: An *Arabidopsis* myb homolog is induced by dehydration stress and its gene pro
 A:Reference number: J02390; MUID:94146551
 A:Accession: J02390
 A:Molecule type: mRNA
 A:Residues: 1-273 <STO>
 A:Cross-references: DDBJ:D14712; NID:g455462; PIDN:BA00534.1; PID:g506189
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentley, M.I.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,

euss.D.: Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, A.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A64420; MUID:20083487
 A:Accession: 864912
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-273 <STO>
 A:Cross-references: GSI:AE002093; NID:q2275197; PIDD:AMB63819.1; GSPDH:GN00139
 C:Comment: The expression of the gene encoding for this protein is induced by dehydration
 C:Genetics:
 A:Gene: Atmyb2; AC2947190
 A:Map position: 2
 A:Introns: 53/1: 96/2
 C:Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology
 C:Keywords: DNA binding; duplication
 E:17-69/Domain: myb DNA-binding repeat homology <MYB1>
 E:70-120/Domain: myb DNA-binding repeat homology <MYB2>

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Query Match 100.1%; Score 246; DB 1; Length 273;
Best Local Similarity 76.44; Pred. No. 3.2e-22;
Matches 42; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY      1 PDVRRGNITTEEQLLIMELHAKWGNGNSKIAKHLPGGRDNEIKNFWRRIOKHK 55
      |||||  |||  ::::|  |||||::|:|||||::|:|||||::|:|
Db      71 PDVRRGNITTEEQFWILKTLKHSJLWGNGNSKIAQYLPGRDNEIKNFWRRIOK 125

RESULT  12

T51642
Probable transcription factor MYB21 [Imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
C:Accession: T51642
R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.;
  Paz-Ares, J.; Weisshart, B.
Plant J. 16, 263-276, 1998
A:Title: Towards functional characterisation of the members of the R2R3-MYB gene from Ar
A:Reference number: Z14349; MUID:9939469
A:Accession: T51642
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-141 <RRA>
A:Cross-references: EMBL:AF062870; PIDN:AAC83592.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: MYB21
C:Superfamily: Arabidopsis myb-DNA-binding protein 2; myb DNA-binding repeat homology

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```

Query Match      73.3%  Score 225  DB 2:  length 141;
Best Local Similarity 97.6%  Pred. No. 5.4e-20;
Matches 40;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

QY      16  IMELHAKGCMNRMSKIYAKHLPGRTDNEIKNFWRTRIQKHIQ 56
          |||
Db       1  IMELHAKGCMNRMSKIYAKHLPGRTDNEIKNFWRTRIQKHIQ 41

RESULT  13

T06650
myb-related protein homolog T6C15.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 19-May-2000
C:Accession: T06650
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15791
A:Accession: T06650
A:Molecule type: DNA
A:Residues: 1-261 <BEV>

```

A:Cross-references: EMBL:AL049656; GSPDB:GN00065; ATSP:TP615...30
A:Experimental source: cultivar Columbia; BAC clone T615
C:Genetics:
A:Gene: ATSP:T6G15.30
A:Map position: 4
A:Introns: 39/1; 82/2
C:Superfamily: unassigned myb DNA-binding repeat proteins; myb DNA-binding repeat hom
P:56-106/Domain: myb DNA-binding repeat homology <MYB>

```

Query Match 70.7%; Score 217; DB 2; Length 261;
Best Local Similarity 67.3%; Pred. No. 9,9e-19;
Matches 37; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Oy 1 PDVRGNTTTEBQILIMEIHAKMGNGRMSKIAKHLPGRDNEIKNWRTRIQKHK 55
||:|||||:|:|||||||||||:|||||||||||:|:|
DB 57 PDLKRGQTTPHDESILIELHAKMGNGRMSWTIARSLSPGRDNEIKNWRTRHPKKAK 111

RESULT 14
T51666
myb-related transcription factor MYB59 [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_rev1sion 18-Aug-2000 #text_change 31-Mar-2001
C:Accession: T51666
R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.;
Paz-Ares, J.; Weissenbach, B.
Plant J. 16, 263-276, 1998
A:Title: Towards functional characterisation of the members of the R2R3-MYB gene from
A:Reference number: 214349; MUID:9839469
A:Accession: T51666
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-234 <KRA>
A:Cross-references: EMBL:AF062894; PIDN:AAC83616.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: MYB59
C:Superfamily: Antirrhinum myb-related protein 315; myb DNA-binding repeat homology
C:Keywords: transcription factor

```

RESULT 15
T49254
myb DNA binding protein-like - Arabidopsis thaliana
N:Alternate names: protein F12M12.100
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C:Accession: T49254
R:Jordan, N.; Banerji, S.; Wiedelmann, R.; Voss, H.; Unseid, M.; Mewes, H.W.; Rudd, S.
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25020
A:Accession: T49254
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 (JQOR)
A:Cross-references: EMBL:AL355775; GSPDB:GN00061; ATSP:F12M12.100
A:Experimental source: cultivar Columbia; BAC clone F12M12
C:Genetics:
A:Gene: ATSP:F12M12.100
A:Introns: 40/1, 83/2
A:Map position: 3
C:Superfamily: Anthrithum myb-related protein 315: myb DNA-binding repeat homology

Tue Oct 8 11:32:58 2002

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Query Match Similarity 70.0% Score 215 DB 2: Length 256;
      Local Similarity 62.5% Pred. No 1.7e-19;
Matches 35; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 PDVGRGNTTTEQLIMELAAKMGKRSKIAKHLFGPFDNEFKNWRPRQIQHIQ 56
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 58 PGLKAGKGTPOERELVLELHAAKMGKRSKIAKHLFGPFDNEFKNWRPRRIKRAAE 113
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: October 8, 2002, 09:30:41
Job time: 115 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 8, 2002, 09:30:11 : Search time 43.61 Seconds

(without alignments)
265.760 Million cell updates/sec

Title: US-09-640-211A-2346

Sequence: 1 MDKKPPDDSGKSDQVEVRKG.....AAGLKRTGKSCRRLRWLYLR 67

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_19:*

1: sp.archaea:*

2: sp.bacteria:*

3: sp.fungi:*

4: sp.human:*

5: sp.invertebrate:*

6: sp.mammal:*

7: sp.mhc:*

8: sp.organelle:*

9: sp.phage:*

10: sp.plant:*

11: sp.potent:*

12: sp.virus:*

13: sp.vertebrate:*

14: sp.unclassified:*

15: sp.virus:*

16: sp.bacteriophage:*

17: sp.archaeap:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	305.5	84.2	217	10	P93474
2	304	83.7	205	10	P81391
3	292	80.4	214	10	G9SPG9
4	287	79.1	184	10	G9AVB7
5	287	79.1	198	10	P81396
6	286	78.8	226	10	G22684
7	286	78.8	226	10	G91K95
8	260	71.6	206	10	G9SSA1
9	250.5	69.0	335	10	G39552
10	249	68.6	307	10	G9EGY3
11	248.5	68.5	333	10	G39550
12	248.5	68.5	333	10	G39551
13	246.5	67.9	285	10	G9ARI8
14	241	66.4	243	10	G94CJ3
15	236	65.0	286	10	G9C9G7
16	235	64.7	224	10	G94CZ2

17	234	64.5	216	10	G9FNM0	G9FNM0 arabidopsis
18	232	63.9	341	10	G9FMR4	G9FMR4 oryza sativ
19	230	63.4	283	10	G94PU0	G94PU0 arabidopsis
20	228.5	62.9	323	10	G9LDE1	G9LDE1 arabidopsis
21	228	62.8	293	10	G93V35	G93V35 oryza sativ
22	226	62.3	273	10	G39028	G39028 arabidopsis
23	223	61.4	256	10	G94IG1	G94IG1 arabis gemm
24	223	61.4	273	10	G94IF9	G94IF9 arabidopsis
25	223	61.4	273	10	G94IF8	G94IF8 arabidopsis
26	223	61.4	273	10	G94IF6	G94IF6 arabidopsis
27	223	61.4	273	10	G93VZ0	G93VZ0 arabidopsis
28	223	61.4	273	10	G93V46	G93V46 arabidopsis
29	217	59.8	273	10	G94IF7	G94IF7 arabidopsis
30	216	59.5	269	10	G9LK14	G9LK14 arabidopsis
31	215	59.2	261	10	G9T0G9	G9T0G9 arabidopsis
32	214	59.0	293	10	G94JN5	G94JN5 gossypium h
33	213	58.7	276	10	G9LRU5	G9LRU5 arabidopsis
34	211	58.1	136	10	P92986	P92986 arabidopsis
35	210	57.9	319	10	G9SPG6	G9SPG6 arabidopsis
36	209	57.6	293	10	G94JN4	G94JN4 gossypium h
37	208	57.3	340	10	G9FR07	G9FR07 zea mays su
38	207	57.0	367	10	G9LHY6	G9LHY6 oryza sativ
39	206	56.7	330	10	G9FR08	G9FR08 zea mays su
40	206	56.7	335	10	G9FR09	G9FR09 zea mays (m
41	206	56.7	335	10	G944N2	G944N2 zea mays (m
42	205	56.7	376	10	G24579	G24579 zea mays (m
43	205	56.5	187	10	G94EN3	G94EN3 fragaria an
44	205	56.5	371	10	G22264	G22264 arabidopsis
45	205	56.5	371	10	G9SBG6	G9SBG6 arabidopsis

ALIGNMENTS

RESULT 1

P93474 PRELIMINARY: PRT; 217 AA.

AC P93474:

DT 01-MAY-1997 (TREMBLrel, 03, Created)

DT 01-MAY-1997 (TREMBLrel, 03, Last sequence update)

DT 01-DEC-2001 (TREMBLrel, 19, Last annotation update)

DE MYB26.

OS Pisum sativum (Garden pea).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eustosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.

OC NCBI_TaxID=3888;

RN [1]

RP SEQUENCE FROM N. A.

RC TISSUE=FLOWER BUD;

RX MEDLINE=96112025; PubMed=9450341;

RA Uimari A., Strommer J.;

RT "MYB26: A MYB-like protein of pea flowers with affinity for promoters of phenylpropanoid genes.";

RL Plant J 12:1273-1284(1997).

DR EMBL: Y11105; CAA71992.1; -.

DR HSSP: P01103; IPOM.

DR TRANSFAC: T02874; -.

DR InterPro: IPR001005; MYB_DNA_Bind.

DR Pfam: PF00249; MYB_DNA-binding; 2.

DR SMART: SM00395; SANT; 2.

DR PROSITE: PS00037; MYB_1; UNKNOWN_1.

DR PROSITE: PS00334; MYB_2; 1.

DR PROSITE: PS00090; MYB_3; 2.

SO SEQUENCE 217 AA; 25388 MW; EA101E1B1030149 CRC64;

Query Match 84.2%; Score 305.5; DB 10; Length 217;

Best Local Similarity 88.1%; Prod. No. 5.8e-30;

Matches 59; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

1 MDKKPPDDSGKSDQVEVRKGPWTMEDLLINVIANHGGSGNSLAKAAGLKRTGKSRLL 60

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Db      1 MDKKF-----CNSSQDDEVRRKGPTWMEEDLLINVIANHGGVWNSLAKAAGLRTGKSCRL 57
QY      61 RWLNLYLR 67
        |||||||
Db      58 RWLNLYLR 64

RESULT  2
P81391  PRELIMINARY:      PRT;      205 AA.
ID      P81391
AC      P81391;
DT      01-JUN-1998 (TREMBLrel. 06, Created)
DT      01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      MYB-RELATED PROTEIN 305.
GN      MYB 305.
OS      Antirrhinum majus (Garden snapdragon).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots;
OC      Asteridae; eumasterids I; Lamiales; Veroniceae; Antirrhinum.
OX      NCBI_TaxID=4151;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=J1522; TISSUE=FLOWER BUDS;
RX      MEDLINE=93005689; PubMed=1840903;
RA      Jackson D., Cullineez-Macia F., Piescott A.G., Roberts K., Martin C.;
        *Expression patterns of myb genes from Antirrhinum flowers.*;
RT      Plant Cell 3:115-125(1991).
CC      1- FUNCTION: MAY BE A TRANSCRIPTIONAL ACTIVATOR.
CC      1- TISSUE SPECIFICITY: MATURE FLOWER.
CC      1- DEVELOPMENTAL STAGE: FIRST DETECTED IN 15-20 MM BUDS.
CC      1- SIMILARITY: BELONGS TO THE MYB FAMILY OF PROTEINS.
DR      PIR; J00958; J00958.
DR      HSSP; P01103; 1POM.
DR      TRANSFAC; T02907; -.
DR      InterPro; IPR001395; Aldo_ket_red.
DR      InterPro; IPR001005; Myb_DNA_bind.
DR      Pfam; PF00249; Myb_DNA-binding; 2.
DR      SMART; SM00395; SANT; 2.
DR      PROSITE; PS00063; ALDO-KETO-REDUCTASE_3; UNKNOWN_1.
DR      PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR      PROSITE; PS00334; MYB_2; 1.
DR      PROSITE; PS00900; MYB_3; 2.
KM      Nuclear protein; DNA-binding; Repeat; Transcription regulation.
FT      DNA_BIND 10 62
FT      MYB.
FT      FT 63 103
FT      DNA_BIND 63 103
SQ      SEQUENCE 205 AA; 23507 MW; A0B1315BA7C309CB CRC64;

Query Match      83.7%; Score 304; DB 10; Length 205;
Best Local Similarity 86.6%; Pred. No. 8.4e-30;
Matches 58; Conservative 3; Mismatches 2; Indels 4; Gaps 1.

OY      1 MDKKRDDSGKQDVEVRKGPTWMEEDLLINVIANHGGVWNSLAKAAGLRTGKSCRL 60
DB      1 MDKKKCN-----SQDVEVRKGPTWMEEDLLINVIANHGGVWNSLARSAGLRTGKSCRL 56
        |||||||
OY      61 RWLNLYLR 67
        |||||||
DB      57 RWLNLYLR 63

RESULT  3
O9SPG9  PRELIMINARY:      PRT;      214 AA.
ID      O9SPG9
AC      O9SPG9;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      PUTATIVE TRANSCRIPTION FACTOR.
DE      MYB24.
GN      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RX MEDLINE=99056848; PubMed=9839469;
RA Kranz H.D., Denckamp M., Greco R., Jin H., Leyva A., Meissner R.C.,
RA Petroni C., Urzainqui A., Bevan M., Martin C., Smeekens S.,
RA Tonelli C., Paz-Ares J., Weissbar B.;
RT "Towards functional characterisation of the members of the R2R3-MYB
RT gene family from Arabidopsis thaliana.";
RL Plant J. 16:263-276(1998).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RA Stracke R., Weissbar B.;
RT "R2R3-MYB transcription factor gene nomenclature in Arabidopsis
RT thaliana.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98069011; PubMed=9405937;
RA Kocant H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
RT Sequence features of the regions of 1,044,062 bp covered by thirteen
RT physically assigned P1 clones.";
RL DNA Res. 4:291-300(1997).
DR EMBL; AF175987; AAD53092.1; -.
DR EMBL; AB006702; BAB11590.1; -.
DR HSSP; P01103; IPOM.
DR InterPro: IPR001395; Aldo_ket_red.
DR InterPro: IPR01005; MYB_DNA_bind.
DR Pfam: PF00249; myb_DNA-binding; 2.
DR SMART; SM00385; SANT; 2.
DR PROSITE; PS00063; ALDO_KETO_REDUCTASE_3; UNKNOWN_1.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00940; MYB_3; 2.
SO SEQUENCE 214 AA; 24459 MW; B5DAE2471F75673F CRC64;

Query Match 80.4%; Score 292; DB 10; Length 214;
Best Local Similarity 80.6%; Pred. No. 2.7e-28;
Matches 54; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY 1 MDRKDDDSGKSQDVEVRKGPWTMEDLLIYIANHGGSSNSLAKAAGLRTGKSCRL 60
Db 1 MEKRSGGSGSGDAEVRKGPWTMEDLLIYIANHGGGVNSLAKSGLKRTGKSCRL 60
OY 61 RLNLNLYR 67
Db 61 RLNLNLYR 67

RESULT 4
O9AVB7 PRELIMINARY; PRT; 184 AA.
AC O9AVB7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LHMVY PROTEIN.
DE LHMV.
OS Liliium hybrid division I.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Liliium.
NCBI_TaxID=156532;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=CV, MONTREUX; TISSUE=TEPAL;

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RC STRAIN=COLUMBIA;
 RX MEDLINE=20363099; PubMed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
 RT TAC and BAC clones.";
 RL DNA Res. 7:217-221(2000).
 DR EMBL; AF000371; BAB02527.1; JOINED.
 DR HSSP; P01103; IPOM.
 DR InterPro: IPR001005; Myb_DNA_bind.
 DR Pfam; PF00249; myb_DNA-binding; 2.
 DR SMART; SM00395; SANT; 2.
 DR PROSITE; PS00063; ALDORETU_REDUCTASE_3; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 SQ SEQUENCE 226 AA; 25351 MW; D29479EBFDID59CC CRC64;

Query Match 78.8%; Score 286; DB 10; Length 226;
 Best Local Similarity 88.1%; Pred. No. 1.6e-27;
 Matches 52; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 9 SGRSQDVEVRKGPWTMEEDLILYINAHGSGWNSLAKAAGLRKTKSRLRLNLTNR 67
 DB 12 SGRSAEAEVRKGPWTMEEDLILYINAHGSGWNSLAKAAGLRKTKSRLRLNLTNR 70

RESULT 8
 Q9SSA1 PRELIMINARY; PRT; 206 AA.
 AC Q9SSA1;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE POTATIVE TRANSCRIPTION FACTOR.
 GN FAP13.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
 RA Rensing C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Niernm W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome III BAC F4P13 genomic sequence.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC009325; AAF01538.1; -.
 DR HSSP; P01103; IPOM.
 DR InterPro: IPR001005; Myb_DNA_bind.
 DR Pfam; PF00249; myb_DNA-binding; 2.
 DR SMART; SM00395; SANT; 2.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 SQ SEQUENCE 206 AA; 23717 MW; 61DC2A28674D87F7 CRC64;

Query Match 71.6%; Score 260; DB 10; Length 206;
 Best Local Similarity 79.7%; Pred. No. 2.5e-24;
 Matches 47; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 9 SGRSQDVEVRKGPWTMEEDLILYINAHGSGWNSLAKAAGLRKTKSRLRLNLTNR 67
 DB 17 SGRSEBGTVRKGPWTMEEDLILYINAHGSGWNSLAKAAGLRKTKSRLRLNLTNR 75

RESULT 9

Q39552
 ID Q39552 PRELIMINARY; PRT; 335 AA.
 AC Q39552;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE CPM7.
 GN CPM7.
 OS Craterostigma plantagineum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eusterids I; Lamiales; Lamiales incertae sedis; Toreniceae;
 OC Craterostigma.
 OX NCBI_TaxID=4153;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97134962; PubMed=8980522;
 RA Iturriaga G., Leyns L., Villagas A., Charalbeh R., Salamini F.,
 RA Bartels D.;
 RT "A family of novel myb-related genes from the resurrection plant
 RT Craterostigma plantagineum are specifically expressed in callus and
 RT roots in response to ABA or desiccation.";
 RL Plant Mol. Biol. 32:707-716(1996).
 DR EMBL; U33917; AAB58314.1; -.
 DR HSSP; P01103; IPOM.
 DR TRANSFAC; T02881; -.
 DR InterPro: IPR001005; Myb_DNA_bind.
 DR Pfam; PF00249; myb_DNA-binding; 2.
 DR SMART; SM00395; SANT; 2.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 SQ SEQUENCE 335 AA; 38258 MW; 85537EB4F52A6AA3 CRC64;

Query Match 69.0%; Score 250.5; DB 10; Length 335;
 Best Local Similarity 67.2%; Pred. No. 6.7e-23;
 Matches 45; Conservative 10; Mismatches 7; Indels 5; Gaps 1;

OY 1 MDKPPDDSGKSDVEVRKGPWTMEEDLILYINAHGSGWNSLAKAAGLRKTKSRL 60
 DB 15 INSEDDDDSS-----DLRGPWTVEDLFLYINAHGSGWNSLARFAGLRKTKSRL 69

OY 61 RMLNLTNR 67
 DB 70 RMLNLTNR 76

RESULT 10
 Q9FGY3 PRELIMINARY; PRT; 307 AA.
 ID Q9FGY3
 AC Q9FGY3;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE MYB-RELATED TRANSCRIPTION FACTOR.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones.";
 RL DNA Res. 7:31-63(2000).
 DR EMBL; AB023033; BAB10776.1; -.
 DR HSSP; P01103; IPOM.


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SO PROSITE: PS50090; MYB_3: 2.  
DB SEQUENCE 285 AA; 32783 MW; 546E764AA3CA1Dd6 CXC64:  
  
Query Match          67.9%; Score 246.5; DB 10; Length 285;  
Best Local Similarity 67.7%; Pred. No. 1.7e-22;  
Matches 44; Conservative 10; Mismatches 2; Indels 7; Gaps 1;  
  
QY 10 KKSQD-----VEVRKGPWTMEEDLIILINTIANHGSGSWNSLARAAGIKRTGSKCRLRW 62  
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 15 GEQGEFAAAELSSAVLRGRPMWVDEDLTINYSIDHGGGRMVALARAAGIKRTGSKCRLRW 74  
  
OY      63 LNYLR 67  
       |||||  
Db     75 LNYLR 79  
  
RESULT 14  
09ACJ3 PRELIMINARY: PRT: 243 AA.  
AC 09ACJ3.  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE PURATIVE TRANSCRIPTION FACTOR MYB12.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurossids II; Brassicales; Brassicaceae; Arabidopsits.  
OX NCBI_Taxid=3702;  
[1]  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21481677; PubMed=11597504;  
RA Stracke R., Werber M., Weisshar B.;  
RT "The R2R3-MYB gene family in Arabidopsis thaliana." ;  
RL Curr. Opin. Plant Biol. 4:447-456(2001).  
DR EMBL: AY008377; AAC38379.2; -  
SQ SEQUENCE 243 AA; 28292 MW; 7FE9B1D643FBD12E CRC64:  
  
Query Match          66.4%; Score 241; DB 10; Length 243;  
Best Local Similarity 61.5%; Pred. No. 6.9e-22;  
Matches 40; Conservative 15; Mismatches 10; Indels 0; Gaps 0;  
  
QY 3 KKPDSDSGRSODVEVRKGPWTMEEDLIILINTIANHGSGSWNSLARAAGIKRTGSKCRLRW 62  
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 18 KEVEVEVEKKEMIEIRGRPMWVEEDMKLVSYISLHGGRWNLSRSAGLNRTGSKCRLRW 77  
  
OY      63 LNYLR 67  
       |||||  
Db     78 LNYLR 82  
  
RESULT 15  
09CG97 PRELIMINARY: PRT: 286 AA.  
ID 09CG97  
AC 09CG97;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE PURATIVE TRANSCRIPTION FACTOR.  
GN T2ZE19.5.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurossids II; Brassicales; Brassicaceae; Arabidopsits.  
OX NCBI_Taxid=3702;  
[1]  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RX MEDLINE=21016719; PubMed=11130712;  
RA White O.S., Alonso J., Altif R., Palm C.J., Federspiel N.A., Kaul S.,  
RA White O., Alonso J., Altif R., Araujo R., Bowman C.L., Brooks S.Y.,
```

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Cressy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Peng J.-D., Fong B., Fujii C.Y.,
RA Gull J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaytin E.,
RA Kilm C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A.A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maltl R., Marshall A.,
RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
RT Sequence and analysis of chromosome 1 of the plant *Arabidopsis*
RT *thaliana*.
RL Nature 408: 816-820 (2000).
DR EMBL: AC016447; AGG52612.1. -.
DR HSSP: P06876; IMBG.
DR InterPro: IPR001005; MYB_DNA_bind.
DR Pfam: PF00249; myb_DNA-binding; 2.
DR SMART: SM00395; SANT. 3.
DR PROSITE: PS50090; MYB 3. 2.
SO SEQUENCE 286 AA; 33239 MW; C6765A6B744CC717 CRC64;

Query Match 75.0% Score 236 DB 10; Length 286;
 Best Local Similarity 60.2% Pred. No. 3.5e-21;
 Matches 40; Conservative 10; Mismatches 7; Indels 0; Gaps 0.

Search completed: October 8, 2002, 09:36:44
Job time: 393 sec

Theologian A. Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
